

FIG. 1

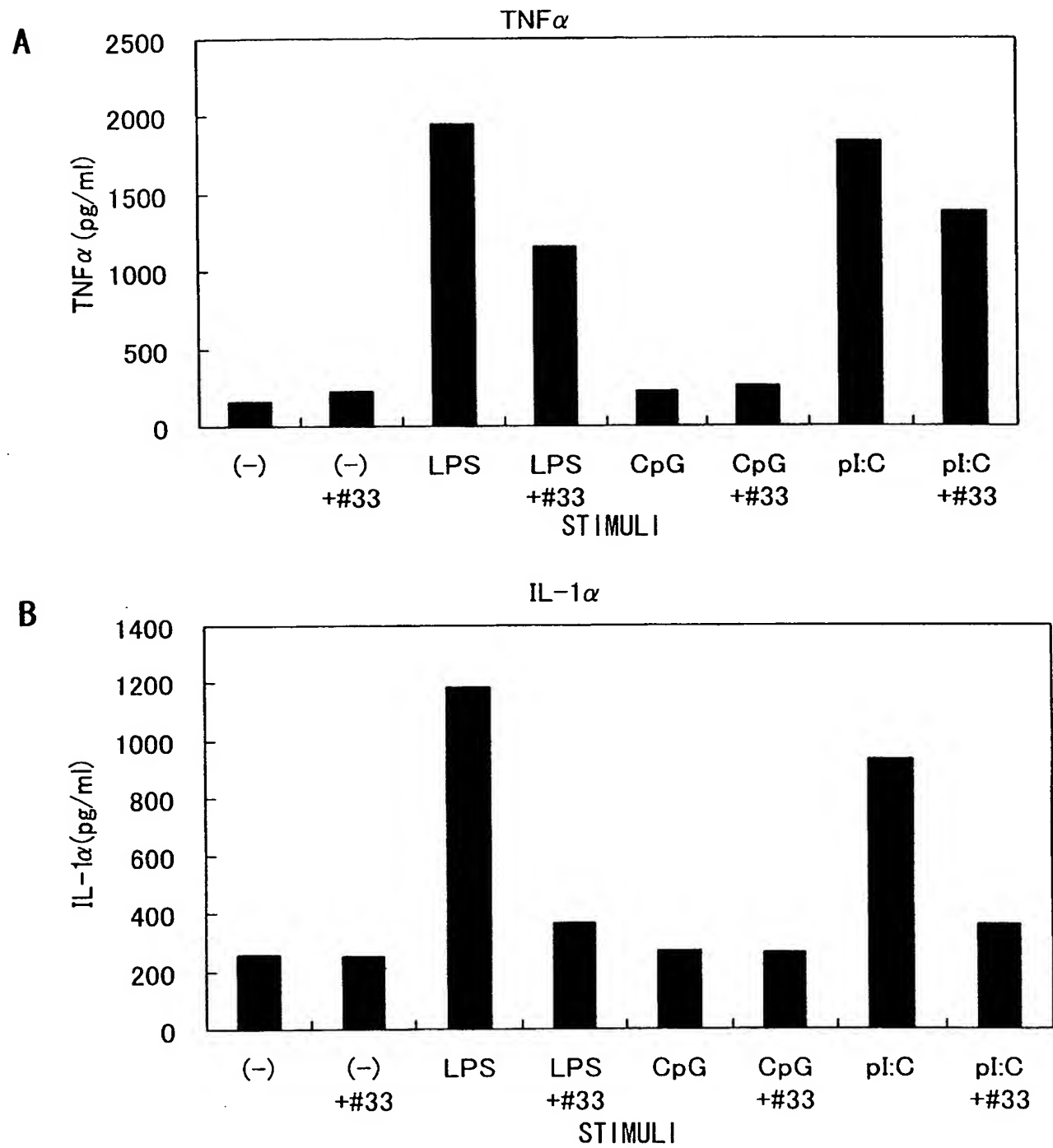


FIG. 2

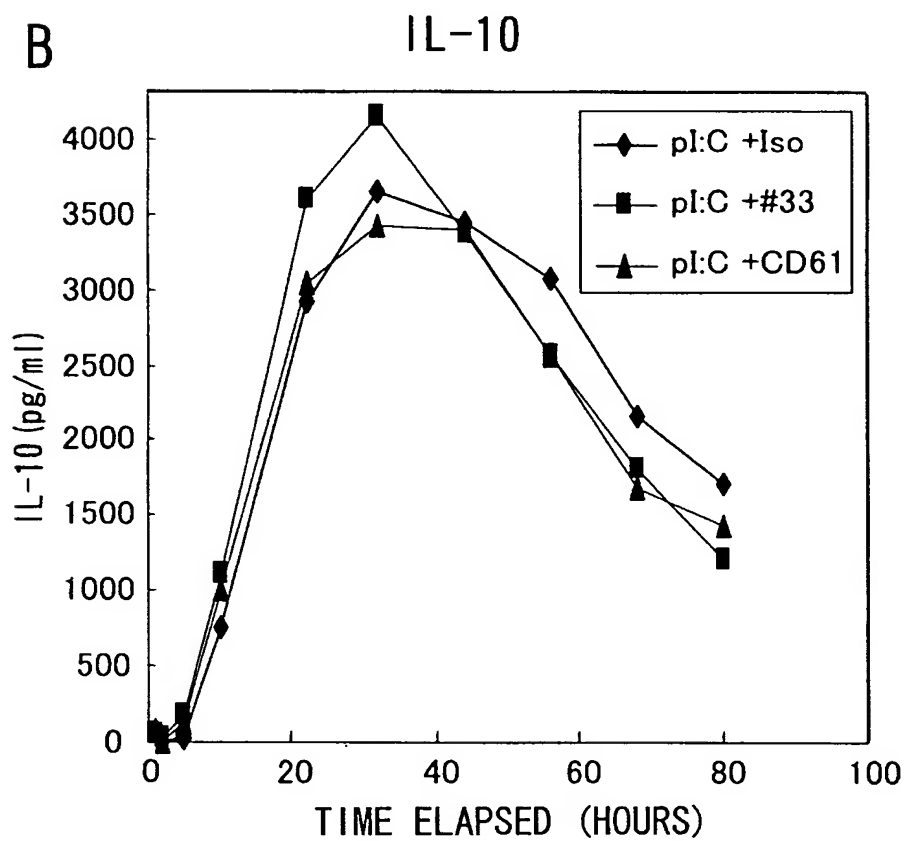
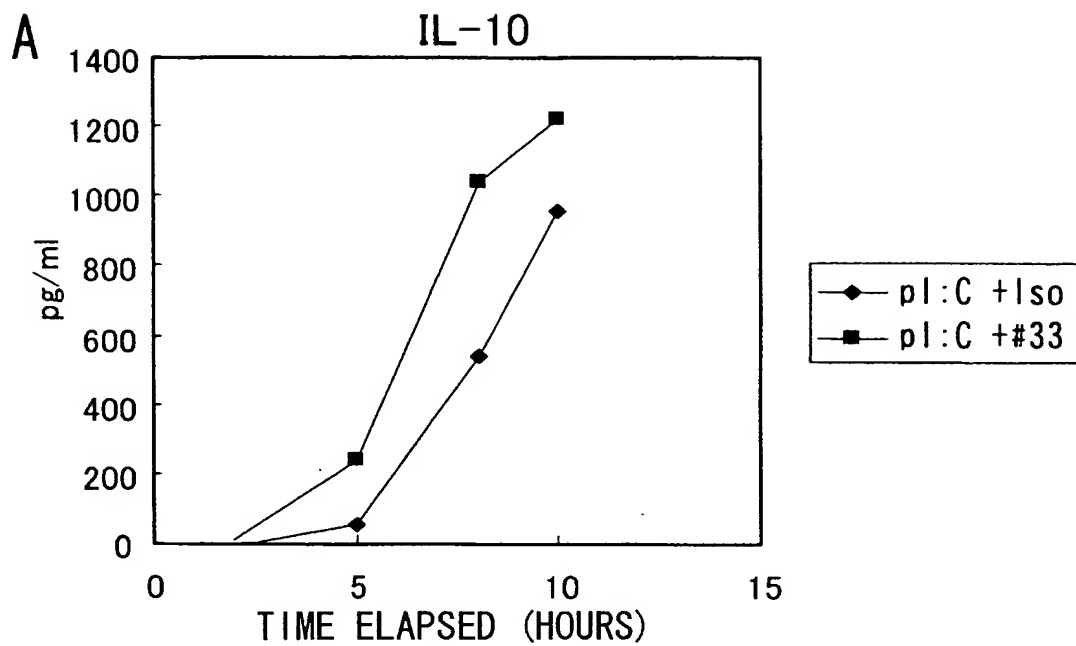


FIG. 3

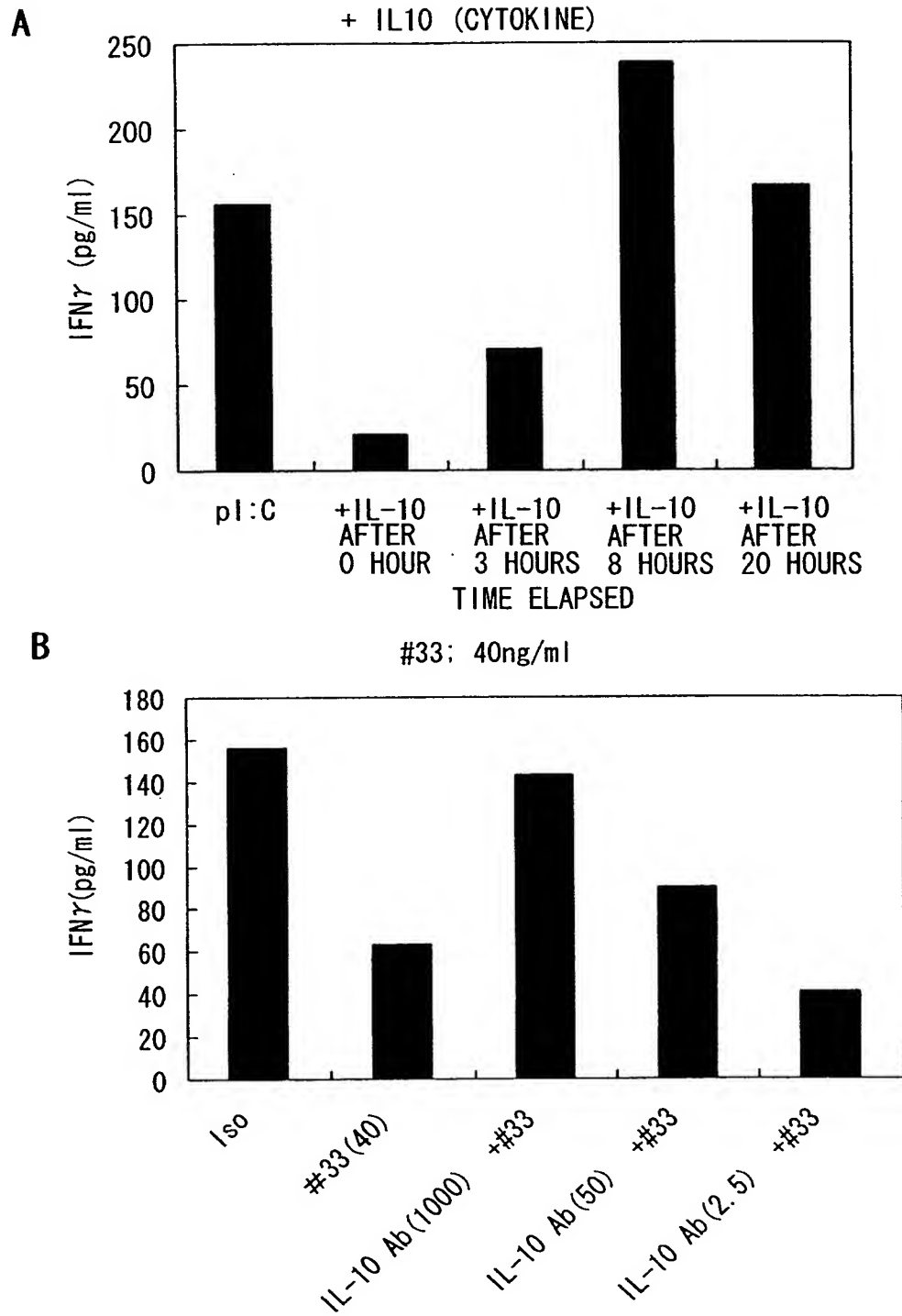


FIG. 4

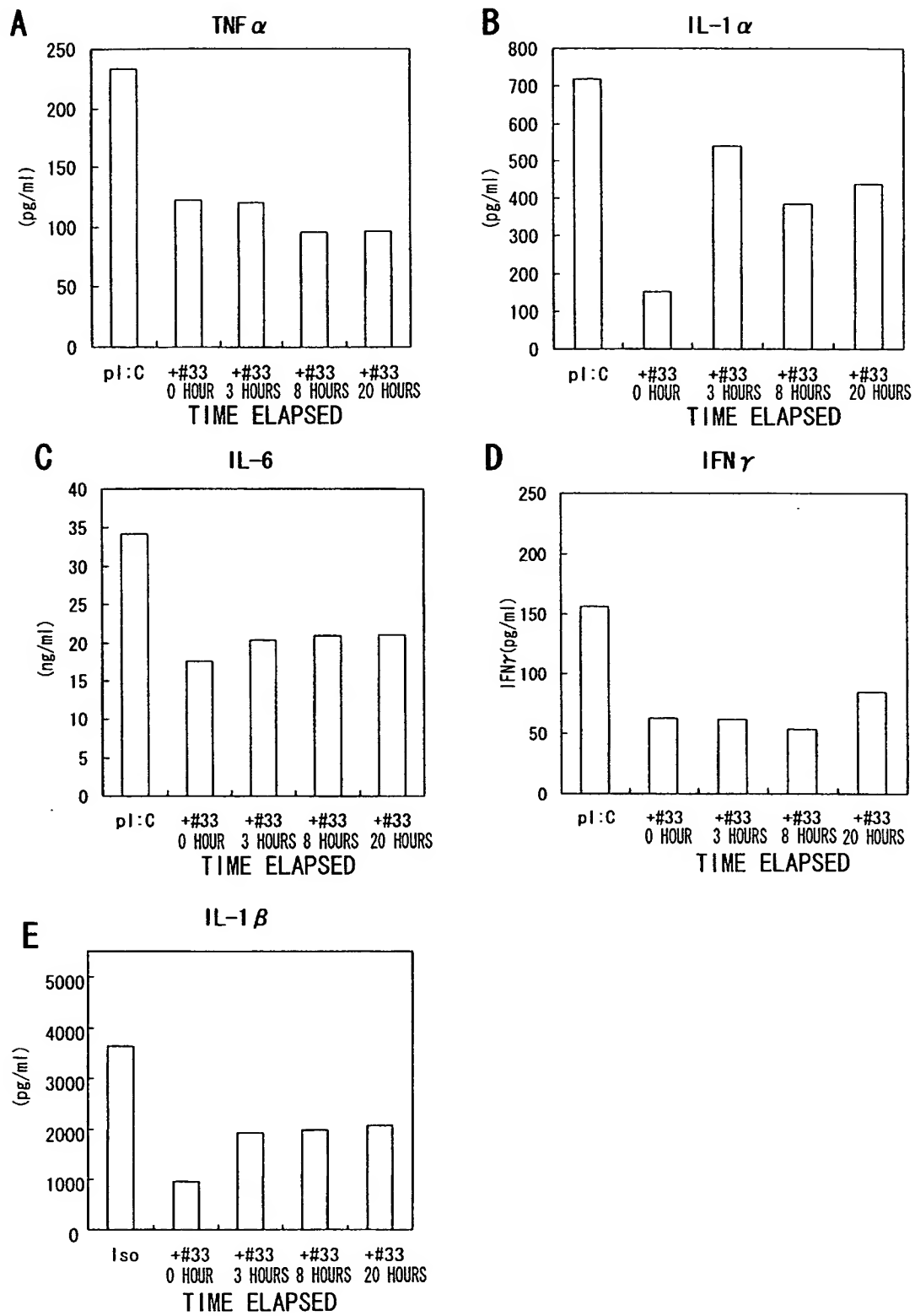


FIG. 5

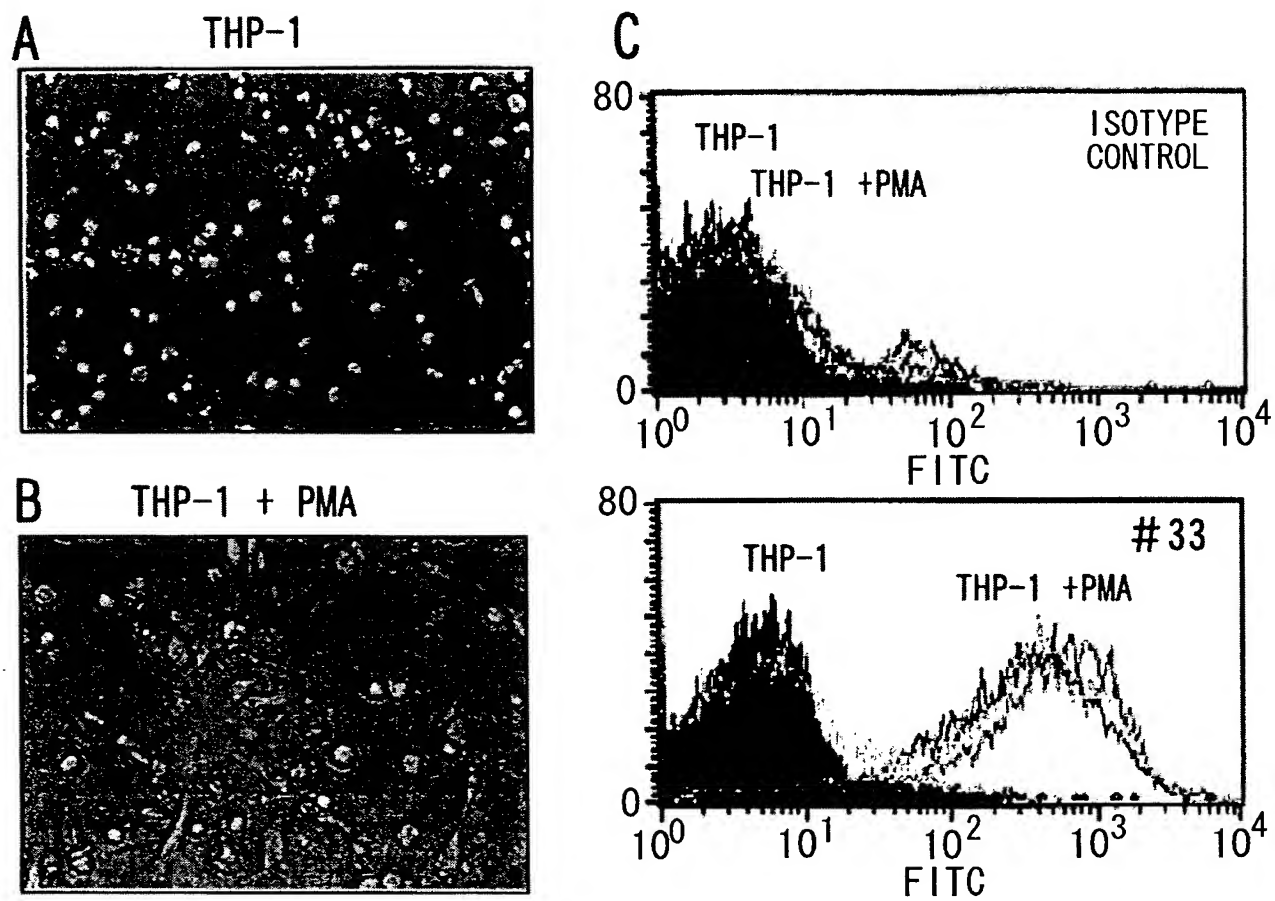


FIG. 6

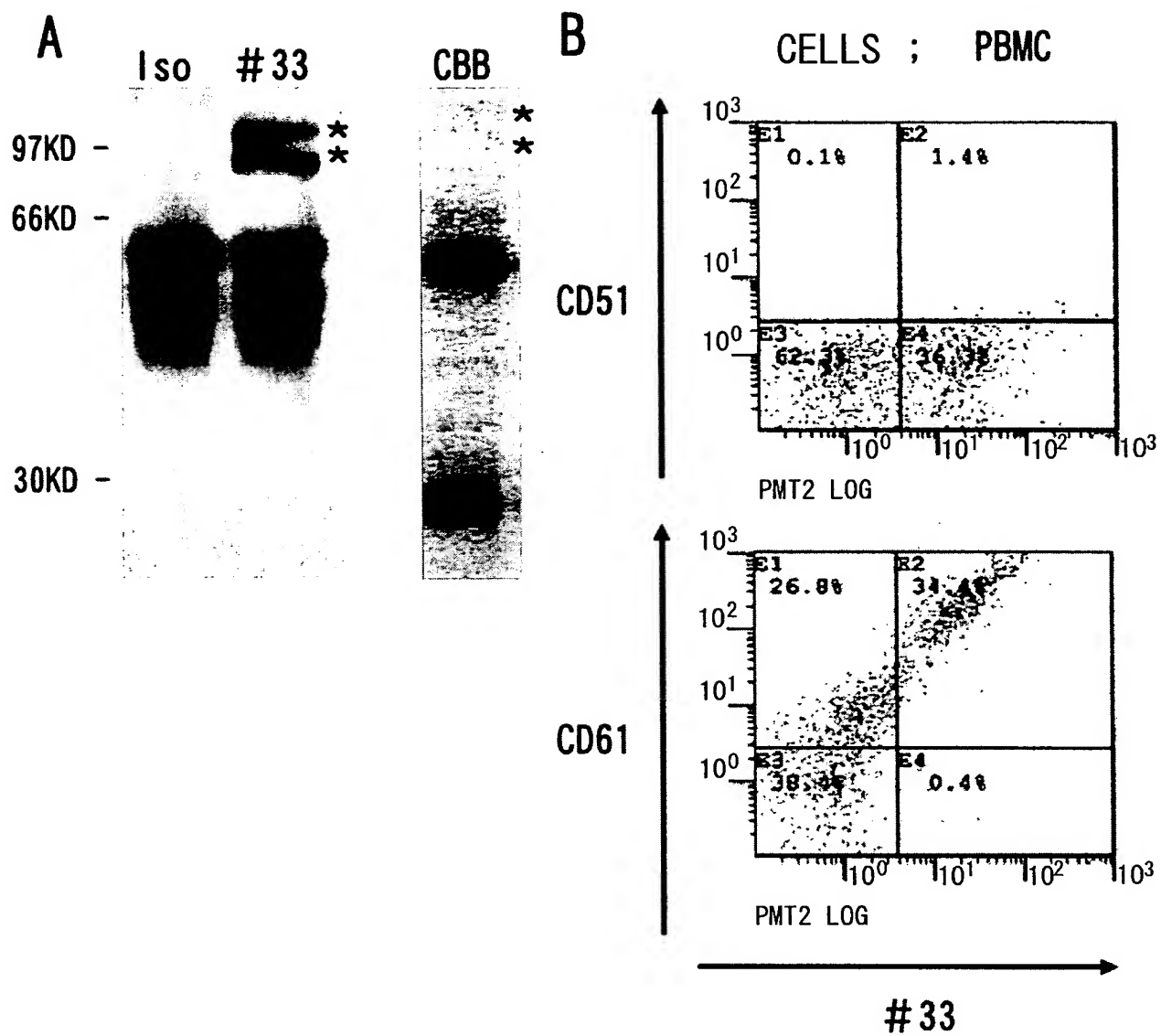


FIG. 7

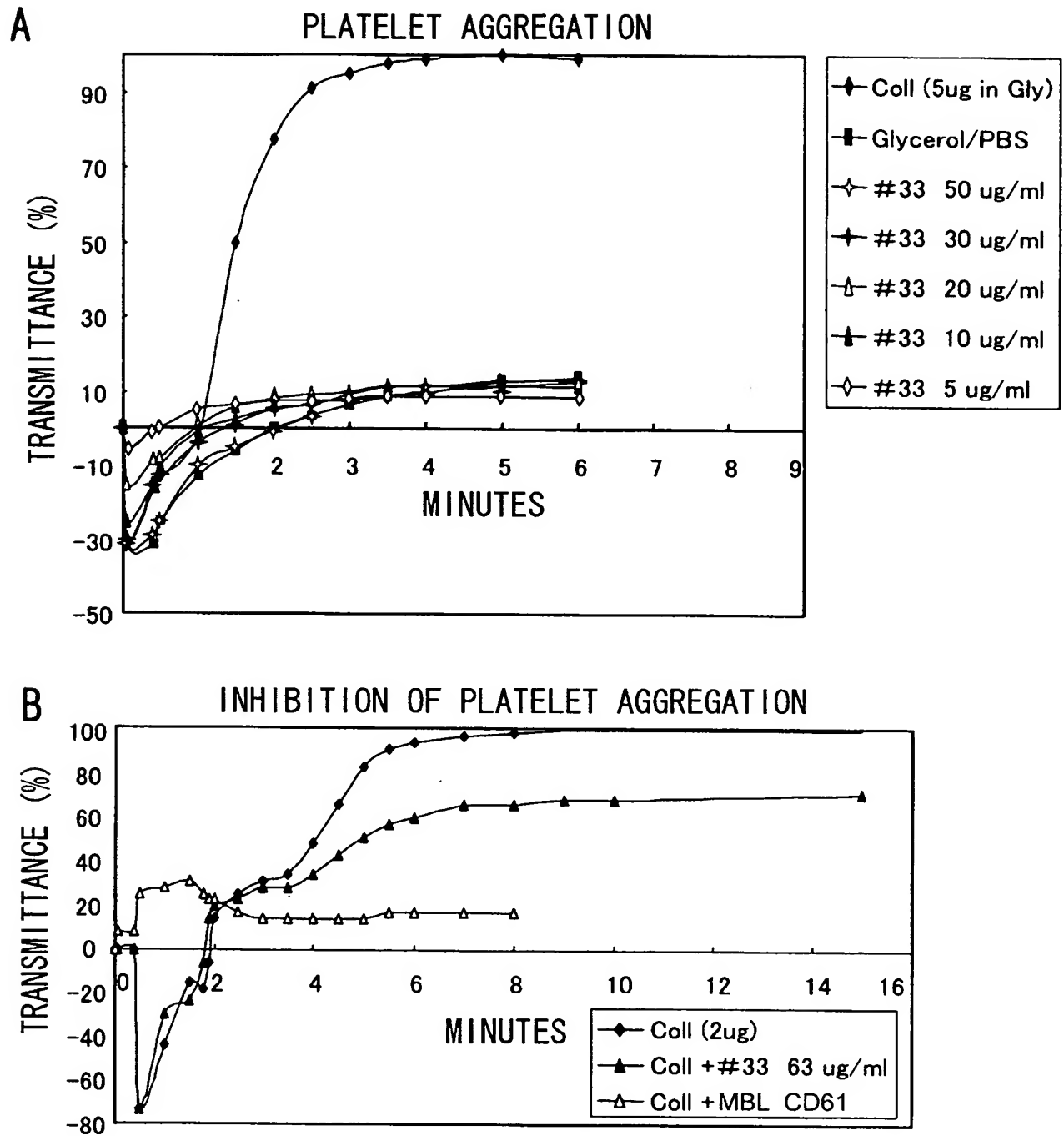


FIG. 8

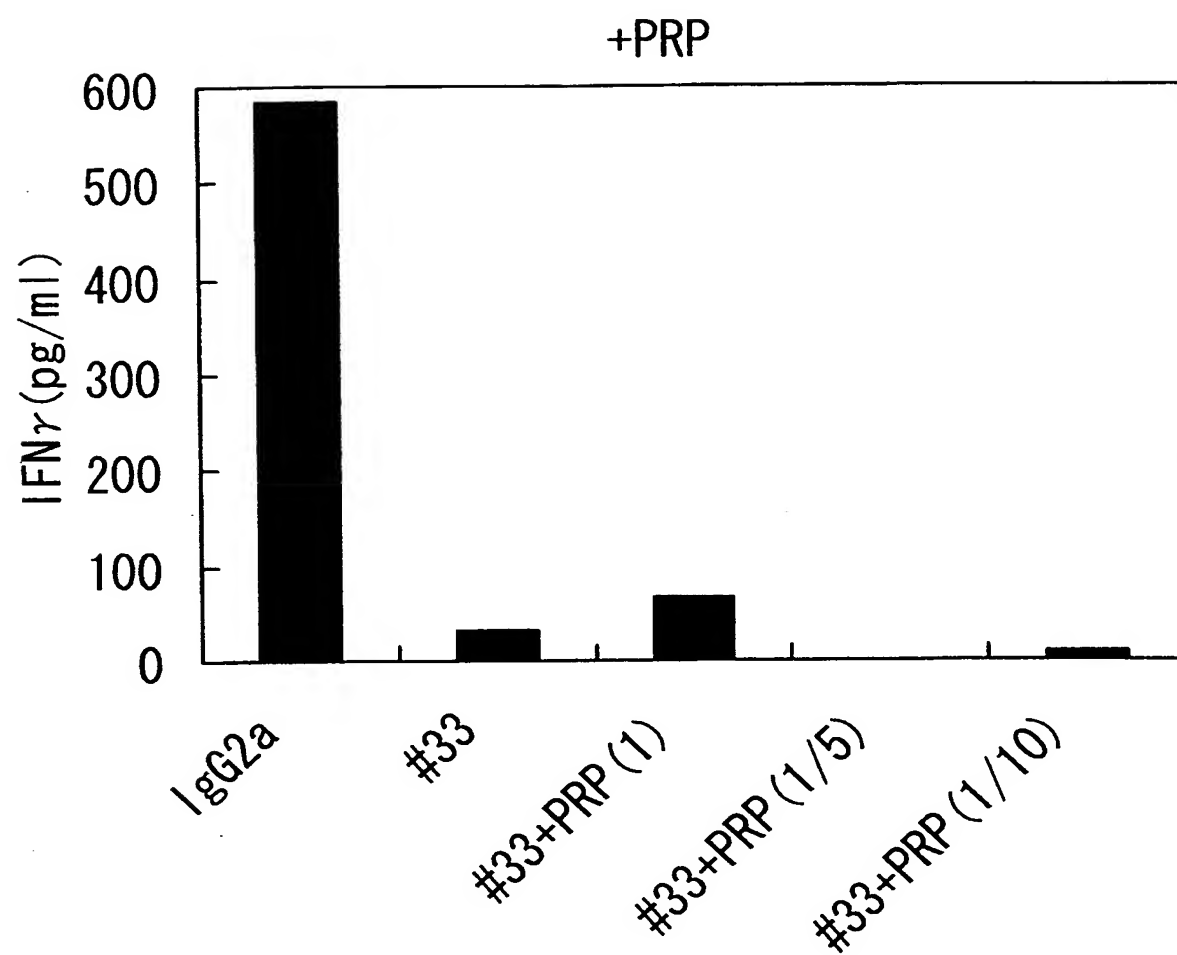


FIG. 9

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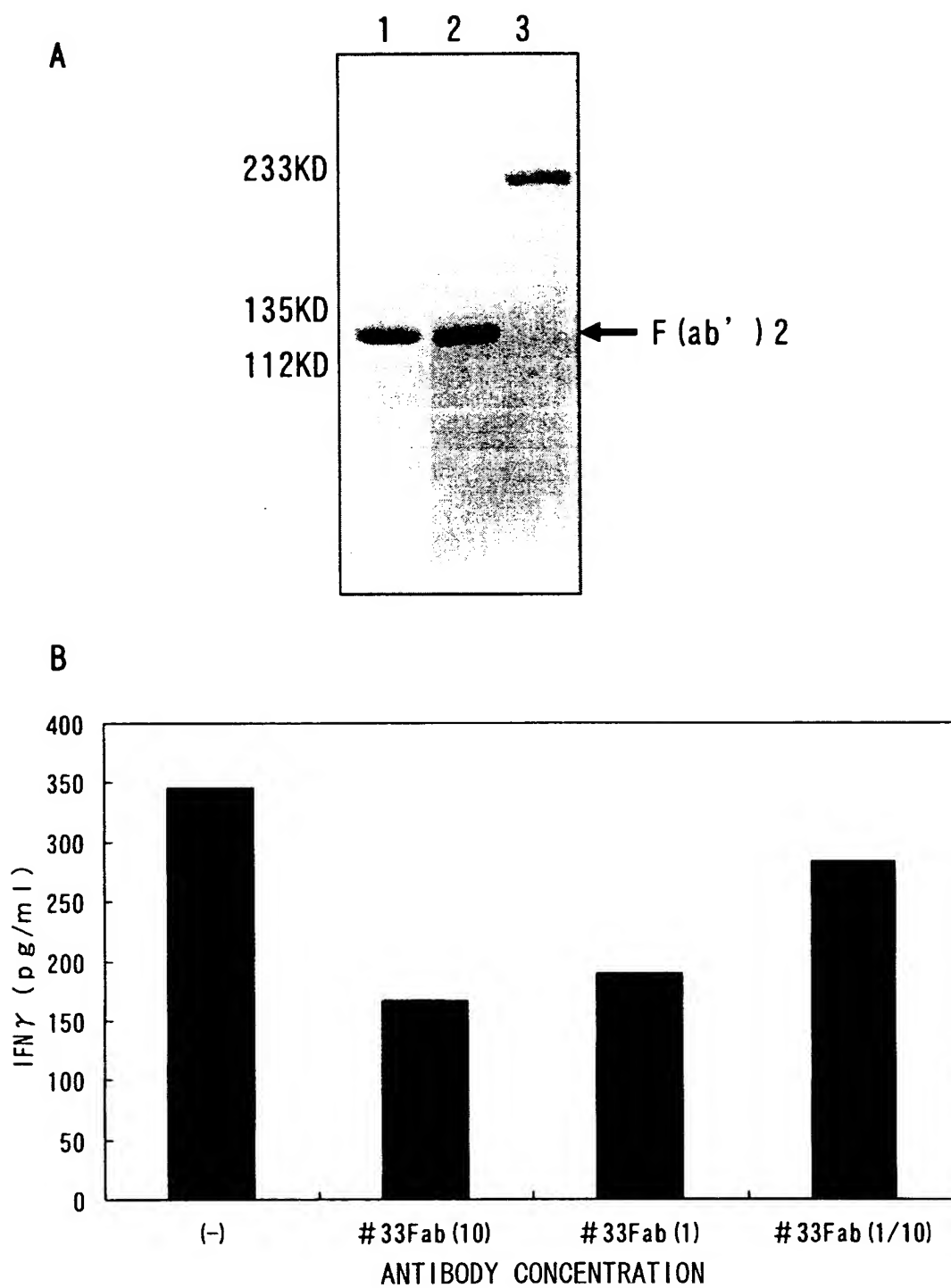


FIG. 10

#33 HEAVY CHAIN								
10	20	30	40	50	60			
ATGGAATGGAGCGGGTCTTTATCTTCCTCCTGTCAGGAACTACAGGTGTCCACTCTGAG								
M	E	W	S	G	V			
F	I	F	L	L	S			
G	T	T	G	V	H			
S	E							
70	80	90	100	110	120			
GTCCAGCTGCTACAGTCTGGACCTGAGCTGGTGAAGCCTGGAGCTTCAATGAAGATATCC								
V	Q	L	L	Q	S			
G	P	E	L	V	K			
P	G	A	S	M	K			
I	S							
130	140	150	CDR1	160	170			
180								
TGCAAGGCTTCTGGTTACTCATTCACTGGCTACACCATGAACTGGGTGAAGCAGAGCCAT								
C	K	A	S	G	Y			
S	F	T	G	Y	T			
M	N	W	V	K	Q			
S	H							
190	200	210	CDR2	220	230			
240								
GGAAAGAACCTTGAGTGGATTGGACTTATTAATCCTTACAGTGGTGTACTACCTACAAC								
G	K	N	L	E	W			
I	G	L	I	N	P			
Y	S	G	V	T	T			
Y	N							
250	260	270	280	290	300			
CAGAGGTTCAAGGGCAAGGCCACATTAAGTGTAGACAAGTCATCCAGCACAGCCTACATG								
Q	R	F	K	G	K			
A	T	L	T	V	D			
K	S	S	S	T	A			
Y	M							
310	320	330	340	350	360			
GAGCTCCTCAGTCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAACACGGGGGGCT								
E	L	L	S	L	T			
S	E	D	S	A	V			
Y	Y	C	A	T	R			
G	A							
370	CDR3	380	390	400	410			
420								
CTGGGACAGGCGTACTACTTTGACTACTGGGGCCAAGGCACCACTCTCACAGTCTCCTCA								
L	G	Q	A	Y	Y			
F	D	Y	W	G	Q			
G	T	T	L	T	V			
S	S							
430	440	450						
GCCAAAACAACAGCCCCATCGGTCTATCCACTG (SEQ ID NO: 12)								
A K T T A P S V Y P L (SEQ ID NO: 4)								

FIG. 11

#33 LIGHT CHAIN																			
10	20	30	40	50	60														
ATGGATTTACAGGTGCAGATTATCAGCTTCCTGCTAATCAGTGCCTCAGTCATGATTTC																			
M	D	L	Q	V	Q	I	I	S	F	L	L	I	S	A	S	V	M	I	S
70	80	90	100	110	120														
AGAGGACAAATTGTTCTCACCCAGTCTCCAGTTATCATGTCTGCATCTCCTGGGGAGAGG																			
R	G	Q	I	V	L	T	Q	S	P	V	I	M	S	A	S	P	G	E	R
130	140	CDR1	150	160	170	180													
GTCACCTTGACCTGCAGTGCCAGCTCAAGTGTAATTACATGCACTGGTACCAGCAGAAG																			
V	T	L	T	C	S	A	S	S	S	V	N	Y	M	H	W	Y	Q	Q	K
190	200	210	CDR2	220	230	240													
TCAGGCACCTCCCCCAAAGATGGATTTATGACACATCCAACTGGCTTCTGGAGTCCCT																			
S	G	T	S	P	K	R	W	I	Y	D	T	S	K	L	A	S	G	V	P
250	260	270	280	290	300														
CCTCGCTTCAGTGGCAGTGGGTTcGGGACATCATACTCTCTCACAATCACCAACATGGAG																			
P	R	F	S	G	S	G	F	G	T	S	Y	S	L	T	I	T	N	M	E
310	320	330	CDR3	340	350	360													
GCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTAGTAAGCCACCCACGTTCCGGT																			
A	E	D	A	A	T	Y	Y	C	Q	Q	W	S	S	K	P	P	T	F	G
370	380	390	400	410	420														
TTTGGGACCAAGCTGGAGCTGCAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCCA																			
F	G	T	K	L	E	L	Q	R	A	D	A	A	P	T	V	S	I	F	P
430																			
CCATCCAGT (SEQ ID NO: 16)																			
P S S (SEQ ID NO: 8)																			

FIG. 12